



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 148565

TO: Nita M Minnifield
Location: 3c01 / 3c18
Wednesday, March 23, 2005
Art Unit: 1646
Phone: 571-272-0860
Serial Number: 09 / 830839

From: Jan Delaval
Location: Biotech-Chem Library
Remsen 1a51
Phone: 571-272-22504

jan.delaval@uspto.gov

Search Notes

From: Chan, Christina
Sent: Tuesday, March 22, 2005 4:36 PM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: interference search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Minnifield, Nita
Sent: Tuesday, March 22, 2005 4:34 PM
To: Chan, Christina
Subject: interference search

Christina, please approve, 2 month amdt.

STIC

09/830839

Please do an interference sequence search on SEQ ID NO:1 and 6 of the above application.

Please provide a paper copy of the results.

Thanks,
Minnifield
71976
Art Unit 1645

RECEIVED
MAR 22 2005
STIC

STAFF USE ONLY

Searcher: [Signature]
Searcher Phone: 212504
Date Searcher Picked up: 3/23/05
Date Completed: 3/23/05
Searcher Prep/Rev. Time: 76
Online Time: 60

Type of Search

NA#: _____ AA#: ✓
Interference: ✓ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: ✓
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: March 23, 2005, 06:57:56 ; Search time 93.5 Seconds
(without alignments)
53.118 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77

Sequence: 1 WNFAGIEAASAIQ 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	15	14	US-10-079-167-80
2	77	100.0	15	5	US-10-345-000-2
3	77	100.0	20	9	US-09-813-333-60
4	77	100.0	20	13	US-10-044-703-60
5	77	100.0	20	11	US-10-239-103-60
6	77	100.0	51	11	US-09-886-349A-33
7	77	100.0	51	14	US-10-193-000-99
8	77	100.0	51	14	US-10-084-843-104
9	77	100.0	51	14	US-10-098-732A-33
10	77	100.0	95	9	US-09-805-427A-1
11	77	100.0	95	16	US-10-333-512A-12
12	77	100.0	95	16	US-10-333-512A-12
13	100.0	403	9	9	US-09-791-171-173

14	77	100.0	403	9	US-09-805-427A-4	Sequence 4, Appli
15	77	100.0	403	10	US-09-804-980-173	Sequence 173, App
16	77	100.0	403	11	US-09-872-505-4	Sequence 4, Appli
17	77	100.0	403	16	US-10-620-246-173	Sequence 173, App
18	77	100.0	404	9	US-09-791-171-172	Sequence 172, App
19	77	100.0	404	9	US-09-805-427A-3	Sequence 3, Appli
20	77	100.0	404	10	US-09-804-980-172	Sequence 172, App
21	77	100.0	404	11	US-09-872-505-3	Sequence 172, App
22	77	100.0	404	16	US-10-620-246-172	Sequence 172, App
23	66	85.7	20	9	US-09-813-333-61	Sequence 61, Appli
24	66	85.7	20	13	US-10-044-703-61	Sequence 61, Appli
25	66	85.7	20	15	US-10-239-103-61	Sequence 59, Appli
26	60	77.9	13	9	US-09-813-333-59	Sequence 59, Appli
27	60	77.9	13	13	US-10-044-703-59	Sequence 59, Appli
28	60	77.9	13	15	US-10-239-103-59	Sequence 59, Appli
29	54	70.1	15	15	US-10-079-167-79	Sequence 79, Appli
30	54	70.1	15	15	US-10-345-000-1	Sequence 1, Appli
31	43	55.8	324	16	US-10-767-701-40957	Sequence 40957, A
32	43	55.8	400	15	US-10-369-493-21850	Sequence 21850, A
33	42.5	55.2	141	15	US-10-389-647-560	Sequence 560, App
34	42	54.5	409	15	US-10-289-762-554	Sequence 554, App
35	42	54.5	1447	16	US-10-437-963-133273	Sequence 133273, A
36	41	53.2	93	16	US-10-437-963-108079	Sequence 108079, A
37	41	53.2	149	15	US-10-264-213-168	Sequence 168, App
38	41	53.2	282	14	US-10-288-930-113	Sequence 113, App
39	41	53.2	443	15	US-10-369-493-9058	Sequence 9058, App
40	41	53.2	445	15	US-10-282-122A-76999	Sequence 76999, A
41	41	53.2	463	14	US-10-156-761-12653	Sequence 12653, A
42	41	53.2	528	15	US-10-282-122A-50764	Sequence 50764, A
43	41	53.2	893	16	US-10-282-122A-69721	Sequence 69721, A
44	40	51.9	419	15	US-10-437-963-168592	Sequence 168592, A
45	40	51.9	934	16	US-10-437-963-164110	Sequence 164110, A

ALIGNMENTS

RESULT 1
US-10-079-167-80
Sequence 80, Application US/10079167
Publication No. US20030138454A1
GENERAL INFORMATION:
APPLICANT: Hill, Adrian V.S.
APPLICANT: McShane, Helen
APPLICANT: Gilbert, Sarah C.
APPLICANT: Reece, William
TITLE OF INVENTION: Vaccination Method
FILE REFERENCE: 2907.1000-001
CURRENT APPLICATION NUMBER: US/10/079,167
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/454,204
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: PCT/GB98/01681
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: GB 97 11957.2
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/GB01/04116
PRIOR FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: GB 00 23203.3
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 80
LENGTH: 15
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: T cell epitope in ESAT6
US-10-079-167-80
Query Match 100.0%; Score 77; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;

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OM protein - protein search, using sw model

Run on: March 23, 2005, 06:36:09 ; Search time 30.5 Seconds
(without alignments)
36.713 Million cell updates/sec

Title: US-09-830-839-1
Perfect score: 79
Sequence: 1 MTEQOMNFAGIEAIA 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	51	US-08-818-112-104	Sequence 104, App
2	79	100.0	51	US-08-818-111-99	Sequence 99, App
3	79	100.0	51	US-09-056-556-104	Sequence 104, App
4	79	100.0	51	US-09-072-596-99	Sequence 99, App
5	79	100.0	51	US-09-072-567-104	Sequence 104, App
6	79	100.0	95	US-08-465-640-2	Sequence 2, App
7	79	100.0	403	US-09-050-739-173	Sequence 173, App
8	79	100.0	404	US-09-050-739-172	Sequence 172, App
9	52	65.8	10	US-09-001-984C-77	Sequence 77, App
10	52	65.8	10	US-09-386-347F-77	Sequence 77, App
11	42	53.2	409	US-09-198-452A-554	Sequence 554, App
12	42	53.2	413	US-08-579-667-4	Sequence 4, App
13	42	53.2	413	US-09-438-185A-515	Sequence 515, App
14	42	53.2	578	US-09-949-016-9799	Sequence 9799, App
15	41	51.9	176	US-09-462-842-3	Sequence 3, App
16	41	51.9	176	US-09-393-171-3	Sequence 3, App
17	40	49.6	295	US-09-602-777A-416	Sequence 416, App
18	39	49.4	538	US-09-252-991A-18026	Sequence 18026, A
19	39	49.4	928	US-09-252-991A-24200	Sequence 24200, A
20	38	48.1	155	US-08-685-808-3	Sequence 3, App
21	38	48.1	155	US-08-505-808C-3	Sequence 3, App
22	38	48.1	339	US-09-489-039A-13578	Sequence 13578, A
23	38	48.1	410	US-08-579-667-2	Sequence 2, App
24	38	48.1	410	US-08-579-667-6	Sequence 6, App
25	38	48.1	410	US-08-579-667-8	Sequence 8, App
26	38	48.1	795	US-09-252-991A-30635	Sequence 30635, A
27	38	48.1	2293	US-09-368-590-2	Sequence 2, App

28	38	48.1	2600	4	US-09-949-016-7309	Sequence 7309, App
29	37	46.8	331	4	US-09-489-039A-9639	Sequence 9639, App
30	37	46.8	435	4	US-09-252-991A-23220	Sequence 23220, A
31	37	46.8	493	4	US-09-540-236-2120	Sequence 2120, App
32	37	46.8	668	4	US-09-538-092-599	Sequence 599, App
33	37	46.8	820	4	US-09-134-000C-6437	Sequence 6437, App
34	36.5	46.2	934	1	US-08-215-805A-80	Sequence 80, App
35	36	45.6	88	4	US-09-270-767-33601	Sequence 33601, A
36	36	45.6	88	4	US-09-270-767-48818	Sequence 48818, A
37	36	45.6	149	4	US-09-634-238-265	Sequence 265, App
38	36	45.6	149	4	US-09-489-039A-8963	Sequence 8963, App
39	36	45.6	221	4	US-09-904-615-155	Sequence 155, App
40	36	45.6	282	4	US-09-724-623-113	Sequence 113, App
41	36	45.6	376	4	US-09-270-957-4	Sequence 4, App
42	36	45.6	376	4	US-09-270-957-19	Sequence 19, App
43	36	45.6	470	4	US-09-502-540-9896	Sequence 9896, App
44	36	45.6	602	3	US-09-149-727-2	Sequence 2, App
45	36	45.6	602	4	US-09-270-957-2	Sequence 2, App

ALIGNMENTS

RESULT 1
US-08-818-112-104
Sequence 104, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NUMBER OF INVENTION: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
State: Washington
Country: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-104
Query Match 100.0%; Score 79; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using SW model

Run on: March 23, 2005, 06:57:56 ; Search time 93.5 Seconds
(without alignments)
53.118 Million cell updates/sec

Title: US-09-830-839-1

Perfect score: 79

Sequence: 1 MTEQGMNFRAGIEAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues
Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
9:	/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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13:	/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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19:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	15	US-10-079-167-79	Sequence 79, Appl
2	79	100.0	15	US-10-345-000-1	Sequence 1, Appl
3	79	100.0	51	US-09-886-349A-33	Sequence 33, Appl
4	79	100.0	51	US-10-193-002-99	Sequence 99, Appl
5	79	100.0	51	US-10-084-843-104	Sequence 104, Appl
6	79	100.0	51	US-10-098-732A-33	Sequence 33, Appl
7	79	100.0	95	US-09-805-427A-1	Sequence 1, Appl
8	79	100.0	95	US-09-872-505-1	Sequence 12, Appl
9	79	100.0	95	US-10-333-512A-12	Sequence 173, Appl
10	79	100.0	403	US-09-791-171-113	Sequence 4, Appl
11	79	100.0	403	US-09-805-427A-4	Sequence 173, Appl
12	79	100.0	403	US-09-804-980-173	Sequence 4, Appl
13	79	100.0	403	US-09-872-505-4	Sequence 4, Appl

14	79	100.0	403	16	US-10-620-246-173	Sequence 173, App
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16	79	100.0	404	9	US-09-805-427A-3	Sequence 3, Appl
17	79	100.0	404	10	US-09-804-980-172	Sequence 172, App
18	79	100.0	404	11	US-09-872-505-3	Sequence 3, Appl
19	79	100.0	404	16	US-10-620-246-172	Sequence 172, App
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21	59	74.7	20	13	US-10-044-703-60	Sequence 60, Appl
22	59	74.7	20	13	US-10-239-103-60	Sequence 60, Appl
23	54	68.4	15	14	US-10-079-167-80	Sequence 80, Appl
24	54	68.4	15	15	US-10-345-000-2	Sequence 2, Appl
25	48	60.8	13	9	US-09-813-333-59	Sequence 69, Appl
26	43	54.4	13	13	US-10-282-122A-69721	Sequence 59, Appl
27	43	54.4	13	13	US-10-044-703-59	Sequence 59, Appl
28	43	54.4	13	15	US-10-239-103-59	Sequence 59, Appl
29	43	54.4	20	9	US-09-813-333-61	Sequence 61, Appl
30	43	54.4	20	13	US-10-044-703-61	Sequence 61, Appl
31	43	54.4	20	15	US-10-239-103-61	Sequence 61, Appl
32	43	54.4	911	15	US-10-282-122A-51365	Sequence 51365, A
33	42	53.2	409	15	US-10-289-762-554	Sequence 554, App
34	42	53.2	539	15	US-10-369-493-16773	Sequence 3, Appl
35	41	51.9	176	14	US-10-339-278-3	Sequence 3, Appl
36	41	51.9	445	15	US-10-282-122A-76999	Sequence 76999, A
37	40	50.6	295	9	US-09-738-626-4782	Sequence 4782, Ap
38	40	50.6	939	15	US-10-282-122A-68011	Sequence 68011, A
39	39	49.4	101	16	US-10-767-701-42935	Sequence 42935, A
40	39	49.4	243	14	US-10-239-663-39	Sequence 39, Appl
41	39	49.4	288	15	US-10-369-493-8029	Sequence 8029, Ap
42	39	49.4	498	15	US-10-425-114-62705	Sequence 62705, A
43	39	49.4	916	9	US-09-815-242-12006	Sequence 12006, A
44	39	49.4	916	15	US-10-282-122A-66644	Sequence 66644, A
45	38	48.1	160	15	US-10-425-114-57412	Sequence 57412, A

ALIGNMENTS

RESULT 1
US-10-079-167-79
Sequence 79, Application US/10079167
Publication No. US20030138454A1
GENERAL INFORMATION:
APPLICANT: Hill, Adrian V.S.
APPLICANT: McShane, Helen
APPLICANT: Gilbert, Sarah C.
APPLICANT: Reece, William
APPLICANT: Schneider, Joerg
TITLE OF INVENTION: Vaccination Method
FILE REFERENCE: 2907.1000-001
CURRENT APPLICATION NUMBER: US/10/079,167
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/454,204
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: PCT/GB98/01681
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: GB 97 11957.2
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/GB01/04116
PRIOR FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: GB 00 23203.3
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 79
LENGTH: 15
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: T cell epitope in ESAT6
US-10-079-167-79
Query Match 100.0%; Score 79; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e-07;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 06:36:09 ; Search time 30.5 Seconds
(without alignments)
36.713 Million cell updates/sec

Title: US-09-830-839-6

Sequence: 1 WNFAGIEMASAIQG 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: Issued Patents AA:*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	51	3	US-08-818-112-104
2	77	100.0	51	3	US-08-818-111-99
3	77	100.0	51	3	US-09-056-556-104
4	77	100.0	51	4	US-09-072-556-99
5	77	100.0	51	4	US-09-072-556-99
6	77	100.0	51	4	US-08-465-640-2
7	77	100.0	403	4	US-09-050-739-173
8	77	100.0	404	4	US-09-050-739-173
9	42.5	55.2	556	4	US-09-252-991A-17793
10	42	54.5	116	4	US-09-902-540-13488
11	42	54.5	409	4	US-09-198-452A-554
12	42	54.5	413	4	US-09-438-185A-515
13	41	53.2	149	4	US-09-634-238-265
14	41	53.2	282	4	US-09-724-623-113
15	40	51.9	2293	3	US-09-368-580-2
16	40	51.9	2600	4	US-09-949-016-7309
17	39	50.6	221	4	US-09-904-615-155
18	39	50.6	413	4	US-09-252-991A-29788
19	39	50.6	1138	4	US-09-489-039A-13574
20	38	49.4	185	4	US-09-489-039A-13574
21	38	49.4	349	4	US-09-489-039A-13578
22	38	49.4	365	4	US-09-252-991A-30166
23	38	49.4	418	3	US-09-202-893B-4
24	38	49.4	435	4	US-09-252-991A-23220
25	37	48.1	209	4	US-09-252-991A-24013
26	37	48.1	360	3	US-09-509-902A-9
27	37	48.1	472	4	US-09-902-540-15461

28	37	48.1	475	4	US-09-252-991A-20838	Sequence 20838, A
29	37	48.1	898	4	US-09-902-540-11561	Sequence 11561, A
30	37	48.1	947	4	US-09-252-991A-21335	Sequence 21335, A
31	37	48.1	981	4	US-09-902-540-9848	Sequence 9848, Ap
32	37	48.1	1138	4	US-09-252-991A-25952	Sequence 25952, A
33	37	48.1	1223	4	US-09-538-092-777	Sequence 777, App
34	36	46.8	294	4	US-09-489-039A-10933	Sequence 10933, A
35	36	46.8	323	4	US-09-489-039A-10986	Sequence 10986, A
36	36	46.8	328	4	US-09-489-039A-10986	Sequence 10986, A
37	36	46.8	368	4	US-09-489-039A-13753	Sequence 13753, A
38	36	46.8	389	4	US-09-489-039A-8540	Sequence 8540, Ap
39	36	46.8	429	4	US-09-134-000C-3817	Sequence 3817, Ap
40	36	46.8	483	4	US-09-489-039A-13018	Sequence 13018, A
41	36	46.8	578	4	US-09-949-016-9799	Sequence 9799, Ap
42	36	46.8	630	4	US-09-248-796A-25512	Sequence 25512, A
43	36	46.8	759	4	US-09-902-540-16161	Sequence 16161, A
44	36	46.8	1534	4	US-09-543-681A-5182	Sequence 5182, Ap
45	35.5	46.1	467	4	US-09-252-991A-29729	Sequence 29729, A

ALIGNMENTS

RESULT 1
US-08-818-112-104
Sequence 104, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yaser A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESS: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4800
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INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-104
Query Match 100.0%; Score 77; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;